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10/735014: SEQ and interference search

Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

Inventor: GODDARD, AUDREY

Please search

SEQ ID NO:83

PRT 431 aa

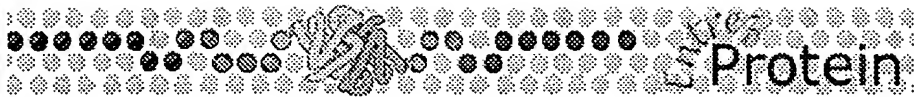
thanks

S.Kaushal

AU1636, REM2.B85

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17:29:41 [309](#)

17:29:32 [2](#)

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Range: from  to 
 Features:
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 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☒ 1: [AAQ88926](#). Reports [FFGG316](#) [Homo sap...[gi:37182248]

[Link, Links](#)

LOCUS AAQ88926 431 aa linear PRI 03-OCT-2003  
 DEFINITION FFGG316 [Homo sapiens].  
 ACCESSION AAQ88926  
 VERSION AAQ88926.1 GI:37182248  
 DBSOURCE accession [AY358563.1](#)  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM [Homo sapiens](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 431)  
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
 PUBMED [12975309](#)  
 REFERENCE 2 (residues 1 to 431)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
 COMMENT Method: conceptual translation.  
 FEATURES  
 Location/Qualifiers  
 source 1..431  
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Protein 1..431  
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CDS 1..431  
 /locus\_tag="UNQ316"  
 /coded\_by="AY358563.1:226..1521"  
 /note="PRO361"

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 61 edcinscst knisgdkacn lmifdtrkta rqpncylffc pneeacplkp aglmsyrii  
 121 tdfpsltrnl psqelpqeds llhgqfsqav tplahhhtdy skptdiswrd tlsqkfgssd  
 181 hlekfkmdc asaqllyake kghsqssqfs sdqeiahlp envsalpatv avasphttsa  
 241 tpkpatllpt nasvtpsgts qpqlattapp vttvtsqppt tlistvftra aatlqamatt  
 301 avlttttfqap tdsksletit pfteisnlit ntgnvynpta lsmsnvesst mnktaswegr  
 361 easpgsssqg svpenqyglp fekwlligsl lfgvflvig lvllgrilse slrrkrysrl  
 421 dylingiyvd i  
 //

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Range: from  to 
 Features:
 ☐ SNP
 ☐ CDS
 ☒ NC
 ☐ HPRD
 ☐ STS

☒ 1: [Q9H8J5](#) Reports MANSC domain cont...[gi:48428493]

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LOCUS Q9H8J5 431 aa linear PRI 01-MAY-2005  
 DEFINITION MANSC domain containing protein 1 precursor (UNQ316/PRO361).  
 ACCESSION Q9H8J5  
 VERSION Q9H8J5 GI:48428493  
 DBSOURCE swissprot: locus MANS1\_HUMAN, accession [Q9H8J5](#);  
 class: standard.  
 extra accessions: Q8NEC1, created: Jul 5, 2004.  
 sequence updated: Jul 5, 2004.  
 annotation updated: May 1, 2005.  
 xrefs: [AK023622.1](#), [BAB14621.1](#), [AY358563.1](#), [AAQ88926.1](#), [BCC32998.2](#),  
[AAH32998.1](#)  
 xrefs (non-sequence databases): Ensembl: ENSG00000111261,  
 Genew: HGNC:25505, InterPro: IPR011106, Pfam: PF07502, PROSITE: PS50986  
 KEYWORDS Glycoprotein; Polymorphism; Signal; Transmembrane.  
 SOURCE Homo sapiens (human)  
 ORGANISM [Homo sapiens](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 431)  
 AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,  
 Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,  
 Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,  
 Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,  
 Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,  
 Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,  
 Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,  
 Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,  
 Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,  
 Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,  
 Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,  
 Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,  
 Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R.,  
 Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,  
 Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,  
 Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,  
 Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,  
 Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,  
 Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,  
 Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,  
 Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,  
 Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,  
 Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,  
 Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,  
 Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,  
 Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,  
 Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,  
 Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,  
 Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.  
 TITLE Complete sequencing and characterization of 21,243 full-length  
 human cDNAs  
 JOURNAL Nat. Genet. 36 (1), 40-45 (2004)  
 PUBMED [14702039](#)  
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 TISSUE=Placenta  
 REFERENCE 2 (residues 1 to 431)  
 AUTHORS Clark, H. F., Gurney, A. L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E.,  
 Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S.,

Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., Godowski, P. and Gray, A.

**TITLE** The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment

**JOURNAL** Genome Res. 13 (10), 2265-2270 (2003)

**PUBMED** [12975309](#)

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

**REFERENCE** 3 (residues 1 to 431)

**AUTHORS** Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

**CONSRTM** Mammalian Gene Collection Program Team

**TITLE** Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

**PUBMED** [12477932](#)

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ILE-55. TISSUE=Testis

**COMMENT** [SUBCELLULAR LOCATION] Type I membrane protein (Potential). [SIMILARITY] Contains 1 MANSC domain.

**FEATURES**

**source** Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

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/gene="MANSC1"

**Protein** 1..431

/gene="MANSC1"

/product="MANSC domain containing protein 1 precursor"

**Region** 1..26

/gene="MANSC1"

/region\_name="Signal"

/note="Potential."

/evidence=not\_experimental

**Region** 27..431

/gene="MANSC1"

/region\_name="Mature chain"

/note="MANSC domain containing protein 1."

/evidence=experimental

**Region** 27..385

/gene="MANSC1"

/region\_name="Domain"

/note="Extracellular (Potential)."

/evidence=not\_experimental

**Region** 33..117

/gene="MANSC1"

/region\_name="Domain"

/note="MANSC."

/evidence=experimental

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/gene="MANSC1"

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/evidence=experimental

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/site\_type="glycosylation"

/note="N-linked (GlcNAc...) (Potential)."

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/evidence=not_experimental
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/site_type="glycosylation"
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Region 237..332

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/gene="MANSC1"
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/note="Thr-rich."
/evidence=experimental
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Site 327

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Site 352

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Region 375

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/evidence=experimental
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ORIGIN

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361 easpgsssqg svpenqyglp fekwlligsf lfgvflfvig lvllgrilse slrrkrysrl
421 dylingiyvd i
//
```

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